

SEQUENCE LISTING

<110> LEUNG, SHAWN SHUI-ON

<120> REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY
FRAMEWORK-PATCHING

<130> SBL-001US

<140> 09/892,613

<141> 2001-06-27

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> FR-patched heavy chain variable region sequence (Full DNA
Sequence) formed by joining the N- and C- terminal (SEQ 3 and 6)
halves at the KpnI site.

<220>

<221> V_region

<222> (1)..(369)

<400> 1

gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgaggctc 60

tcctgtgcag cctctggatt ctccttcagt atctatgaca tgtcttggt tcgccaggca 120

ccggaaagg ggctggagtg ggtcgatac attagtagtg gtgggtgtac cacctactat 180

ccagacactg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac 240

ctgcaaatga acagtctgag ggtggaggac acagccttat attactgtgc aagacatagt 300

ggctacggta gtagctacgg ggtttgttt gcttactggg gccaaaggac tctggtcact 360

gtctcttca 369

<210> 2
<211> 123
<212> PRT
<213> Chimaera sp.

<400> 2
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 111
<212> DNA
<213> Artificial Sequence

<220>

<223> N-template is a synthetic sense-strand oligonucleotide encoding

amino acid 14-50 of the VH region (SEQ ID No. 2). The template is PCR-amplified by two primers (SEQ ID No. 4 and 5)

<220>
<221> V_region
<222> (1)..(111)

<400> 3
cctggagggt ccctgaggct ctcctgtgca gcctctggat ttccttcag tatctatgac 60

atgtcttggg ttcgccaggc accggaaag gggctggagt gggtcgata c 111

<210> 4
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-19 of the VH region (SEQ ID No. 2). The 3' end of the primer overlaps with the 5'end of the template by 18 nucleotides.

<220>
<221> primer_bind
<222> (1)..(57)

<400> 4
gaagtgcagc tgctggagtc tggggaggc tttagtgcagc ctggagggtc cctgagg 57

<210> 5
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 43-59 of the VH region(SEQ ID No. 2). The primer overlaps with the template by 21 nucleotides.

<220>

<221> primer_bind
<222> (1)..(48)

<400> 5
tttaggtggta ccaccaccac tactaatgta tgcgaccac tccagccc 48

<210> 6
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 68-111 of the VH region (SEQ ID No 2) The template is PCR-amplified by two primers (SEQ ID No 7 and 8)

<220>
<221> V_region
<222> (1)..(132)

<400> 6
ttcaccatct ccagagacaa tgccaagaac tccctgtacc tgcaaatgaa cagtctgagg 60
gtggaggaca cagcctata ttactgtgca agacatagtg gctacggtag tagctacggg 120
gttttgttg ct 132

<210> 7
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 55-74 of the VH region (SEQ ID No 2). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(60)

<400> 7
ggtgttacca cctactatcc agacactgtg aaggccgat tcaccatctc cagagacaat 60

<210> 8
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 105-123 of the VH region (SEQ ID No 2). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(57)

<400> 8
tgaagagaca gtgaccagag tcccttgcc ccagtaagca aacaaaaccc cgtagct 57

<210> 9
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FR-patched light chain variable region sequence formed by joining the N- and C- terminal (SEQ 11 and 14) halves at the KpnI site.

<220>
<221> V_region
<222> (1)..(321)

<400> 9
gatatccaga tgacctagtc tccatccccc ctgtctgcct ctgtgggaga cagagtcccc 60

attagttgca gggcaagtca ggacattagc aattatcaa actggtatca gcagaaaccca 120

ggtaaggctc cgaaactcct gatctactac actagtataat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggAACAGAA tttactctca ccattagctc cctgcagcca 240

gaagatttg ccacttactt ttgccaaacag ggtaatacgc ttccgtggac gttcggtgga 300
ggcaccaagg tggaaatcaa a 321

<210> 10
<211> 107
<212> PRT
<213> Chimaera sp.

<400> 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 11
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> N-template is a synthetic sense-strand oligonucleotide encoding

amino acid 11-46 of the VL region (SEQ ID No. 10). The template is PCR-amplified by two primers (SEQ ID No. 12 and 13)

<220>
<221> V_region
<222> (1)..(108)

<400> 11
ctgtctgcct ctgtgggaga cagagtacc attagttgca gggcaagtca ggacattagc 60
aattatttaa actggtatca gcagaaaacca ggtaaggctc cgaaactc 108

<210> 12
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-17 of the VH region (SEQ ID No 10). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(51)

<400> 12
gatatccaga tgacctc tccatcctcc ctgtctgcct ctgtgggaga c 51

<210> 13
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 40-53. The primer and the template overlaps by 18 nucleotides.

<220>

<221> primer_bind
<222> (1)..(40)

<400> 13
atatactagt gtagtagatc aggagttcg gagccttacc

40

<210> 14
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 59-98 of the VH region (SEQ ID No 10) The template is PCR-amplified by tow primers (SEQ ID No 15 and 16)

<220>
<221> V_region
<222> (1)..(120)

<400> 14
ccatcaagg t cagttggcag tgggtctgga acagaattta ctctcaccat tagctccctg 60
cagccagaag attttgccac ttactttgc caacaggta atacgcttcc gtggacgttc 120

<210> 15
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 50-65 of the VH region (SEQ ID No. 10). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides

<220>
<221> primer_bind
<222> (1)..(49)

<400> 15
ctacactagt atattacact caggagtccc atcaagggttc agtggcagt

49

<210> 16
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 92-107 of the VH region (SEQ ID No 10). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(48)

<400> 16
tttgatttcc accttggtgc ctccaccgaa cgtccacgga agcgtatt 48

<210> 17
<211> 371
<212> DNA
<213> Artificial Sequence

<220>
<223> FR-patched heavy chain variable region sequence (Full DNA Sequence) formed by joining the N- and C-terminal (SEQ 19 and 22) halves at the KpnI site.

<220>
<221> V_region
<222> (1)..(371)

<400> 17
caggtcaac tggggcttc cggggctgag gtaaataagc ctggggcctc agtgaaggc 60
tcctgcaagg cttctggcta cacatttacc agttacaata tgcactgggt acggcagcct 120
cctggaaagg gcctggaatg gattggagct atttatccag gaaatggtga tactagttac 180
aatcagaat tcaaggcua ggccacattg actgcagaca aatcctccag cacagcctac 240
atgcagctca gcagtctgac atctgaggac tctgcggctc attactgtgc aagatcgac 300

tacggtagta actacgtaga ctactttgac tactggggcc aaggcaccac tgttacagtc 360

tcctctgatc a 371

<210> 18

<211> 123

<212> PRT

<213> Chimaera sp.

<400> 18

Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Asp
115 120

<210> 19

<211> 114

<212> DNA

<213> Artificial Sequence

<220>

<223> N-template is a synthetic sense-strand oligonucleotide encoding amino acid 12-49 of the VH region (SEQ ID No. 18). The template is PCR-amplified by two primers (SEQ ID No. 20 and 21)

<220>

<221> V_region

<222> (1)..(114)

<400> 19

aataagcctg gggcctcagt gaaggcttcc tgcaaggctt ctggctacac atttaccagt 60

tacaatatgc actgggtacg gcagcctcct ggaaggggcc tggaatggat tgg 114

<210> 20

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-19 of the VH region (SEQ ID No 18). The 3' end of the primer overlaps with the 5'end of the template by 24 nucleotides.

<220>

<221> primer_bind

<222> (1)..(57)

<400> 20

caggtgcaac tggtggttc cggggctgag gtaataagc ctggggcctc agtgaag 57

<210> 21

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide

encoding amino acid 43-60 of the VH region (SEQ ID No 18). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(55)

<400> 21
tgtaactagt atcaccattt cctggataaa tagtccaat ccattccagg cccct 55

<210> 22
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 70-111 of the VH region (SEQ ID No 18) The template is PCR-amplified by tow primers (SEQ ID No 23 and 24)

<220>
<221> V_region
<222> (1)..(126)

<400> 22
ttgactgcag acaaattcctc cagcacagcc tacatgcagc tcagcagtct gacatctgag 60
gactctgcgg tctattactg tgcaagatcg cactacggta gtaactacgt agactacttt 120
gactac 126

<210> 23
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 57-76 of the VH region (SEQ ID No 18). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(61)

<400> 23
tgatactagt tacaatcaga aattcaaggg caaggccaca ttgactgcag acaaatcctc 60
c 61

<210> 24
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 105-123 of the VH region (SEQ ID No 18). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(59)

<400> 24
tgcgtttttt tttttttttt tttttttttt tttttttttt tttttttttt 59
tgtatcagagg agactgtaac agtgggtgcct tggcccccagt agtcaaagta gtctacgta

<210> 25
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FR-patched light chain variable region sequence (Full DNA Sequence) formed by joining the N- and C- terminal (SEQ 27 and 30) halves at the BspEI site.

<220>
<221> V_region
<222> (1)..(321)

<400> 25

gatattcaac tcacacagtc tccatcaagt ctttctgcat ctgtggggga cagagtcaca	60
attacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga	120
tcctccccca aaccctggat ttatgccaca tccaacctgg cttccggagt ccctagtcgc	180
ttcagtggca gtgggtctgg gaccgagttc actctcacaa tcagcagttt gcagcctgaa	240
gatttcgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg	300
accaagctga ccgttctacg g	321

<210> 26

<211> 107

<212> PRT

<213> Chimaera sp.

<400> 26

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly			
1	5	10	15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met		
20	25	30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr		
35	40	45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser		
50	55	60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu			
65	70	75	80

Asp Phe Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr		
85	90	95

Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg	
100	105

<210> 27
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> N-template is a synthetic sense-strand oligonucleotide encoding amino acid 9-51 of the VL region (SEQ ID No. 26). The template is PCR-amplified by two primers (SEQ ID No. 28 and 29)

<220>
<221> V_region
<222> (1)..(129)

<400> 27
tcaagtcttt ctgcatctgt gggggacaga gtcacaattt cttgcaggc cagctcaagt 60
ttaagttca tgcactggta ccagcagaag ccaggatcct cccccaacc ctggatttat 120
gccacatcc 129

<210> 28
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-15 of the VH region (SEQ ID No 26). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(45)

<400> 28
gatattcaac tcacacagtc tccatcaagt ctttctgcat ctgtg 45

<210> 29
<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 45-57. The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(40)

<400> 29
ggactccgga agccaggttg gatgtggcat aaatccaggg 40

<210> 30
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 61-100 of the VH region (SEQ ID No 26) The template is PCR-amplified by tow primers (SEQ ID No 31 and 32)

<220>
<221> V_region
<222> (1)..(120)

<400> 30
ttcagtggca gtgggtctgg gaccgagttc actctcacaa tcagcagttt gcagcctgaa 60
gatttcgcca cttatttctg ccatcagttg agtagtaacc cgctcacgtt cggtgctggg 120

<210> 31
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 54-67 of the VH region (SEQ ID No 18). The 3' end of

the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(43)

<400> 31
ggcttccgga gtccctagtc gcttcagtgg cagtgggtct ggg

43

<210> 32
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 94-107 of the VH region (SEQ ID No 26). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(42)

<400> 32
ccgtagaacg gtcagcttgg tcccagcacc gaacgtgagc gg

42

<210> 33
<211> 123
<212> PRT
<213> Mus sp.

<400> 33
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val

35

40

45

Ala Tyr Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 34
<211> 107
<212> PRT
<213> Mus sp.

<400> 34
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln

65 70 75 80
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 35
<211> 123
<212> PRT
<213> Homo sapiens

<400> 35
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Tyr Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

115

120

<210> 36

<211> 29

<212> PRT

<213> Homo sapiens

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Ala Thr Thr Gly Phe Ala Phe Ser
20 25

<210> 37

<211> 30

<212> PRT

<213> Homo sapiens

<400> 37

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
20 25 30

<210> 38

<211> 30

<212> PRT

<213> Homo sapiens

<400> 38

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
20 25 30

<210> 39

<211> 14
<212> PRT
<213> Homo sapiens

<400> 39
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 40
<211> 32
<212> PRT
<213> Homo sapiens

<400> 40
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg
20 25 30

<210> 41
<211> 11
<212> PRT
<213> Homo sapiens

<400> 41
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr
1 5 10

<210> 42
<211> 107
<212> PRT
<213> Homo sapiens

<400> 42
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 43

<211> 23

<212> PRT

<213> Homo sapiens

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys
20

<210> 44

<211> 15

<212> PRT

<213> Homo sapiens

<400> 44

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 45

<211> 32

<212> PRT

<213> Homo sapiens

<400> 45

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys
20 25 30

<210> 46

<211> 10

<212> PRT

<213> Homo sapiens

<400> 46

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 47

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 47

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 48

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65	70	75	80
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp			
85	90	95	
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys			
100	105		
<210> 49			
<211> 123			
<212> PRT			
<213> Mus sp.			
<400> 49			
Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr			
20	25	30	
Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile			
35	40	45	
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe			
50	55	60	
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr			
65	70	75	80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp			
100	105	110	
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp			

115

120

<210> 50
<211> 107
<212> PRT
<213> Mus sp.

<400> 50
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 51
<211> 123
<212> PRT
<213> Homo sapiens

<400> 51
Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp
115 120

<210> 52

<211> 30

<212> PRT

<213> Homo sapiens

<400> 52

Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 53

<211> 14

<212> PRT

<213> Homo sapiens

<400> 53

Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly
1 5 10

<210> 54

<211> 32

<212> PRT

<213> Homo sapiens

<400> 54

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 55

<211> 32

<212> PRT

<213> Homo sapiens

<400> 55

Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Cys Cys Ala Arg
20 25 30

<210> 56

<211> 11

<212> PRT

<213> Homo sapiens

<400> 56

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 58

<211> 23

<212> PRT

<213> Homo sapiens

<400> 58

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 59
<211> 22
<212> PRT
<213> Homo sapiens

<400> 59
Asn Leu Met Leu Ile Gln Pro Pro Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Met Thr Cys
20

<210> 60
<211> 15
<212> PRT
<213> Homo sapiens

<400> 60
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Pro Val Ile Tyr
1 5 10 15

<210> 61
<211> 32
<212> PRT
<213> Homo sapiens

<400> 61
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys
20 25 30

<210> 62
<211> 32
<212> PRT
<213> Homo sapiens

<400> 62
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

1 5 10 15

Leu Thr Ile Thr Ser Leu Gln Pro Glu Asp Phe Ala Ala Tyr Phe Cys
20 25 30

<210> 63

<211> 32

<212> PRT

<213> Homo sapiens

<400> 63

Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Phe
1 5 10 15

Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Thr Tyr Phe Cys
20 25 30

<210> 64

<211> 32

<212> PRT

<213> Homo sapiens

<400> 64

Gly Val Pro Ala Arg Phe Ser Gly Tyr Asn Ser Gly Asn Ser Ala Phe
1 5 10 15

Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Phe Cys
20 25 30

<210> 65

<211> 11

<212> PRT

<213> Homo sapiens

<400> 65

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1 5 10

<210> 66

<211> 11
<212> PRT
<213> Homo sapiens

<400> 66
Phe Gly Val Gly Ser Lys Val Glu Ser Lys Arg
1 5 10

<210> 67
<211> 11
<212> PRT
<213> Homo sapiens

<400> 67
Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg
1 5 10

<210> 68
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 68
Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 69
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr

85

90

95

Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg
100 105

<210> 70
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 70
Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 71
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Pro Val Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg
100 105